WHAT IS CLAIMED IS:

1. A method of specifying SNP related to disease susceptibility or drug responsiveness and comprising:

a first step of setting a scanning domain beforehand in the base sequence domain that is the object of SNP analysis;

a second step of gradually narrowing down said scanning domain to a localized domain that contains a target SNP; and

a third step of specifying said target SNP from said narrowed down localized domain.

2. The method of specifying SNP of claim 1 wherein said second step comprises a step of setting a marker SNP for specifying said target SNP and gradually narrowing down said scanning domain.

3. The method of specifying SNP of the second claim wherein said second step uses statistical analysis such as haplotype analysis to set said marker SNP.

4. The method of specifying SNP of claim 3 wherein

said first step comprises: a step of setting the scanning domain of said base sequence domain in a genome domain that is limited to genes whose functions are clearly known or chromosomes whose functions can be predicted; and

said second step comprises:

a fourth step of selecting a group of SNP to be typed from said scanning domain and performing SNP typing using a wet process;

a fifth step of finding the probability of appearance of all combinations of said haplotype analysis in said scanning domain based on typing data of said SNP typing as a statistical amount; and

a sixth step of comparing the found said statistical amount with a preset or estimated reference statistical amount, and when there is significant deviation between said statistical amount and said reference statistical amount that exceeds a preset threshold, determining that said marker SNP is contained in the domain corresponding to the deviated position that exceeds said threshold value.

5. The method of specifying SNP of claim 4 wherein said third step comprises:

a seventh step of increasing the specified ratio of the number of SNPs to be the object of typing in the selection of the SNP group in said fourth step when said significant deviation is less than a first threshold value, and then repeating said fifth step;

an eighth step of setting a new scanning domain from said scanning domain that has been decreased by a specified ratio such

that it contains the position of the deviated peak when said significant deviation is greater than said first threshold value but less than a second threshold value, and then repeating said fifth step; and

a ninth step of determining that said marker SNP is contained in the domain corresponding to the deviated position that exceeds said second threshold value when said significant deviation exceeds said second threshold value, setting a new scanning domain from said scanning domain that has been decreased by a specified ratio such that it contains the position of the deviated peak, and then repeating said fifth step.

6. The method of specifying SNP of claim 5 wherein said ninth step comprises a step of setting SNPs that include the target SNP for which all DNA samples are typed when the number of SNPs in a selected group is less then a specified number.

7. The method of specifying SNP of claim 5 wherein said seventh step comprises a step of determining that the target SNP is not contained and stopping the process when the number of times the process of said fifth step is performed exceeds a specified number of times.

8. The method of specifying SNP of claim 5 in which said eighth step comprises a step of determining that the target SNP is not contained and stopping the process when the number of times the process of said fifth step is performed exceeds a specified number of times.

9. The method of specifying SNP of any one of the claims 1 thru 8 wherein said second step comprises a step of typing the SNP using a quality controlled process, and where said quality controlled process performs typing of four SNP on one assay plate for one sample, and determines that the typing data is invalid when the number of typed SNPs found having significant difference by a statistical method such as the Chi-square test exceeds a specified number and identifies the data as being contaminated by contamination of the sample.

10. The method of specifying SNP of claim 9 in which said second step repeats SNP typing only for SNP found to have said significant difference when the number of typed SNPs found to have significant difference was a specified number, and when the result of no significant difference continues for a specified number of times, determines that said typing data is correct and uses that data.

11. A computer program that can be read by a computer that can execute the processing of the method of specifying SNP of any one of the claims 1 thru 10 wherein all of the steps of any one of the claims 1 thru 10 are coded.